

Figure 1a

Variable Heavy Chain DNA

3077_VH1B (SEQ ID NO: 1):

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(1)  CAGGTGCAAT TGGTTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGCGAG
(51) CGTGAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACT TCTTATTCTA
(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAAGTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTTA TTCATGGTAT GCTTGATTTT TGGGGCCAAG GCACCCTGGT
(351) GACGGTTAGC TCA

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3079_VH3 (SEQ ID NO: 2):

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(1)  CAGGTGCAAT TGGTGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTTCT AATTATGGTA
(101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCCGTTCTG ATGGTAGCTG GACCTATTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCATT TCACGTGATA ATTCGAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTCGTTAT
(301) TGGTCTAAGT CTCATGCTTC TGTTACTGAT TATTGGGGCC AAGGCACCCT
(351) GGTGACGGTT AGCTCA

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3080_VH3 (SEQ ID NO: 3):

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(1)  CAGGTGCAAT TGGTGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTTCT TCTTATGGTA
(101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCTATTCTG ATGGTAGCAA TACCTTTTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCATT TCACGTGATA ATTCGAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTAATATG
(301) TATCGTTGGC CTTTTCATTA TTTTTTTGAT TATTGGGGCC AAGGCACCCT
(351) GGTGACGGTT AGCTCA

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3100_VH 3 (SEQ ID NO: 4):

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(1)  CAGGTGCAAT TGGTGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTTCT TCTAATGGTA
(101) TGTCTTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCTCTTATC TTTCTAGCTC TACCTATTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCATT TCACGTGATA ATTCGAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTTTTAT
(301) GGTTATTTTA ATTATGCTGA TGTTTGGGGC CAAGGCACCC TGGTGACGGT
(351) TAGCTCA

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3077_1_VH1B (SEQ ID NO: 31):

```

(1)  CAGGTGCAAT TAGTCCAAAG TGGTGCGGAA GTGAAAAAAC CGGGCGCGAG
(51) CGTGAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACT TCTTATTCTA

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(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAAGTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTTA TTCATGGTAT GCTTGATTTT TGGGGCCAAG GCACCCTGGT
(351) GACGGTTAGC TCA

Figure 1b**Variable Heavy Chain Peptide****(CDR Regions in Bold)****3077_VH1B (SEQ ID NO: 5):**

(1) QVQLVQSGAE VKKPGASVKV SCKASGYTFT **SY**SINWVRQA PGQGLEWMGY
(51) IDPNRGNTNY **AQKFQ**GRVTM TRDTSISTAY MELSSLRSED TAVYYCAREY
(101) **IYFIHGMLDF** WGQGTLVTVS S

3079_VH3 (SEQ ID NO: 6):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS **NYGM**HWVRQA PGKGLEWVSN
(51) IRSDGSWTFY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARRY
(101) WSKSHASVTD YWGQTLVTV SS

3080_VH3 (SEQ ID NO: 7):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS **SYGM**HWVRQA PGKGLEWVSN
(51) **IYSDGSNTFY** ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARNM
(101) YRWPFHYFFD YWGQTLVTV SS

3100_VH 3 (SEQ ID NO: 8):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS **SNGM**SWVRQA PGKGLEWVSN
(51) **ISYLSSSTYY** ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARFY
(101) **GYFNYADVWG** QGTLVTVSS

Figure 2a**Variable Light Chain DNA****3077_Vk kappa 2 (SEQ ID NO: 9):**

```

(1)  GATATCGTGA TGACCCAGAG CCCACTGAGC CTGCCAGTGA CTCCGGGCGA
(51) GCCTGCGAGC ATTAGCTGCA GAAGCAGCCA AAGCCTGCTT TTTATTGATG
(101) GCAATAATTA TCTGAATTGG TACCTTCAAA AACCAGGTCA AAGCCCGCAG
(151) CTATTAATTT ATCTTGGTTC TAATCGTGCC AGTGGGGTCC CGGATCGTTT
(201) TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT AGCCGTGTGG
(251) AAGCTGAAGA CGTGGGCGTG TATTATTGCC AGCAGTATTC TTCTAAGTCT
(301) GCTACCTTTG GCCAGGGTAC GAAAGTTGAA ATTAAACGTA CG

```

3079_Vk kappa 1 (SEQ ID NO: 10):

```

(1)  GATATCCAGA TGACCCAGAG CCCGTCTAGC CTGAGCGCGA GCGTGGGTGA
(51) TCGTGTGACC ATTACCTGCA GAGCGAGCCA GGATATTTCT GCTTTTCTGA
(101) ATTGGTACCA GCAGAAACCA GGTAAAGCAC CGAAACTATT AATTTATAAG
(151) GTTTCTAATT TGCAAAGCGG GGTCCCGTCC CGTTTTAGCG GCTCTGGATC
(201) CGGCACTGAT TTTACCCTGA CCATTAGCAG CCTGCAACCT GAAGACTTTG
(251) CGACTTATTA TTGCCAGCAG GCTTATTCTG GTTCTATTAC CTTTGGCCAG
(301) GGTACGAAAAG TTGAAATTAA ACGTACG

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3080_VI lambda 3 (SEQ ID NO: 11):

```

(1)  GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
(51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTAATAAG TATGTTTCTT
(101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTGTTGTGAT TTATGGTGAT
(151) AATAATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
(201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
(251) ATTATTATTG CTCTTCTTAT GATTCTTCTT ATTTTGTGTT TGGCGGCGGC
(301) ACGAAGTTAA CCGTTCCTTG CCAG

```

3100_VI lambda 3 (SEQ ID NO: 12):

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(1)  GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
(51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTCATTAT TATGCTTCTT
(101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTCTTGTGAT TTATCGTGAT
(151) AATGATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
(201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
(251) ATTATTATTG CCAGTCTTAT GATTATCTTC ATGATTTTGT GTTTGGCGGC
(301) GGCACGAAGT TAACCGTTCT TGGCCAG

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Figure 2b

Variable Light Chain Peptide

(CDR Regions in Bold)

3077_Vk kappa 2 (SEQ ID NO: 13):

(1) DIVMTQSP^{LS} LPVTPGEPAS ISCRSSQ^{SL}L **FIDGNNYL**NW YLQKPGQSPQ
(51) **LLIYL**GSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDGVV **YYCQ**QYSSKS
(101) ATFGQGTKVE IKRT

3079_Vk kappa 1 (SEQ ID NO: 14):

(1) DIQMTQSP^{SS} LSASVGDRVT ITCRASQ^{DIS} **AFLN**WYQ^KKP GKAPKLLIYK
(51) **VSNLQ**SGVPS RFSGSGSGTD FTLTISSLQ^P EDFATYYC^QQ **AYSG**SITFGQ
(101) GTKVEIKRT

3080_Vl lambda 3 (SEQ ID NO: 15):

(1) DIELTQPPSV SVAPGQTARI SCSGDNIGNK **YVSW**YQ^KKPG QAPVVVIYGD
(51) **NNRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC^{SS}Y **DSSY**FVFGGG
(101) TKLTVLGQ

3100_Vl lambda 3 (SEQ ID NO: 16):

(1) DIELTQPPSV SVAPGQTARI SCSGDNIGHY **YASW**YQ^KKPG QAPVLVIYRD
(51) **NDRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC^QSY **DYLH**DFVFGG
(101) GTKLTVLGQ

Figure 3**Variable Heavy Chain Consensus Sequences**(CDR Regions in **Bold**)**VH1B Consensus (SEQ ID NO: 17):**

(1) QVQLVQSGAE VKKPGASVKV SCKASGYTFT **SYMHWVRQA** PGQGLEWMGW
(51) INPNSGGTNY AOKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCARWG
(101) GDGFYAMDYW GQGLVTVSS

VH3 Consensus (SEQ ID NO: 18):

(1) QVQLVESGGG LVQPGGSLRL SCAASGFTFS **SYAMSWVRQA** PGKGLEWVSA
(51) ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARWG
(101) GDGFYAMDYW GQGLVTVS S

Figure 4**Variable Light Chain Consensus Sequences**

(CDR Regions in Bold)

VL_λ3 Consensus (SEQ ID NO: 19):

(1) SYELTQPPSV SVAPGQTARI **SCSGDALGDK** YASWYQQKPG QAPVLVIYDD
(51) **SDRPSGIPER** FSGSNSGNTA TLTISGTQAE DEADYYCQQH YTTTPPVFGGG
(101) TKLTVLG

VL_k1 Consensus (SEQ ID NO: 20):

(1) DIQMTQSPSS LSASVGDRVT ITCRASQGIS **SYLAWYQQKP** GKAPKLLIYA
(51) **ASSLQSGVPS** RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HYYTTPPTFGQ
(101) GTKVEIKR

VL_k2 Consensus (SEQ ID NO: 21):

(1) DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL **HSNGYNYLDW** YLQKPGQSPQ
(51) **LLIYLGSNRA** SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV **YYCQQHYTTP**
(101) PTFGQGTKVE IKR

Figure 5**Peptide Sequence of CD38**

(SEQ ID NO: 22):

```
1    mancefspvs gdkpccrlsr raqlclgvs lvlilvvvla vvvprwrqqw sgpgttkrfp
61   etvlarcvky teihpemrhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpcn
121  killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc
181  snpvsvfwk tvsrrfaaaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvtlea
241  wvihggregs rdlcqdpdik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei
```


Figure 6**Nucleotide Sequence of Chimeric OKT10**

Heavy Chain (SEQ ID NO: 23):

caggtggaat tgggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc
 gatTTTTAGTA gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg
 attggagaaa ttaatccaga tagcagtacg ataaactata cgacatctct aaaggataaa
 ttcacatctt ccagagacaa cgccaaaaat acgctgtacc tgcaaatgac caaagtgaga
 tctgaggaca cagcccttta ttactgtgca agatatggta actggtttcc ttattggggc
 caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggt cttccccctg
 gcacctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac
 tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac
 accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg
 ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcaca gccagcaac
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 tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaacccaag
 gacacctca tgatctcccg gacctctgag gtcacatgcg tgggtgtgga cgtgagccac
 gaagacctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaaag
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 ctgcaccagg actggtgaa tggcaaggag tacaagtgca aggtctcaa caaagccctc
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 aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg
 catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

Light Chain (SEQ ID NO: 24):

gatatcctga tgaccagtc tcaaaaaatc atgccacat cagtgggaga cagggtcagc
 gtcacctgca aggcagtc aaatgtggat actaatgtag cctggatatca acagaaacca

ggacagtctc ctaaagcact gatttactcg gcatcctacc gatacagtgg agtccctgat
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct
gaggacttgg cagagtatct ctgtcagcaa tatgacagct atcctctcac gttcgggtgct
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gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg
ctgagcaaag cagactacga gaaacacaaa gtctacgctt gcgaagtcac ccatcagggc
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

Fig.7: Schematic Overview of Epitopes

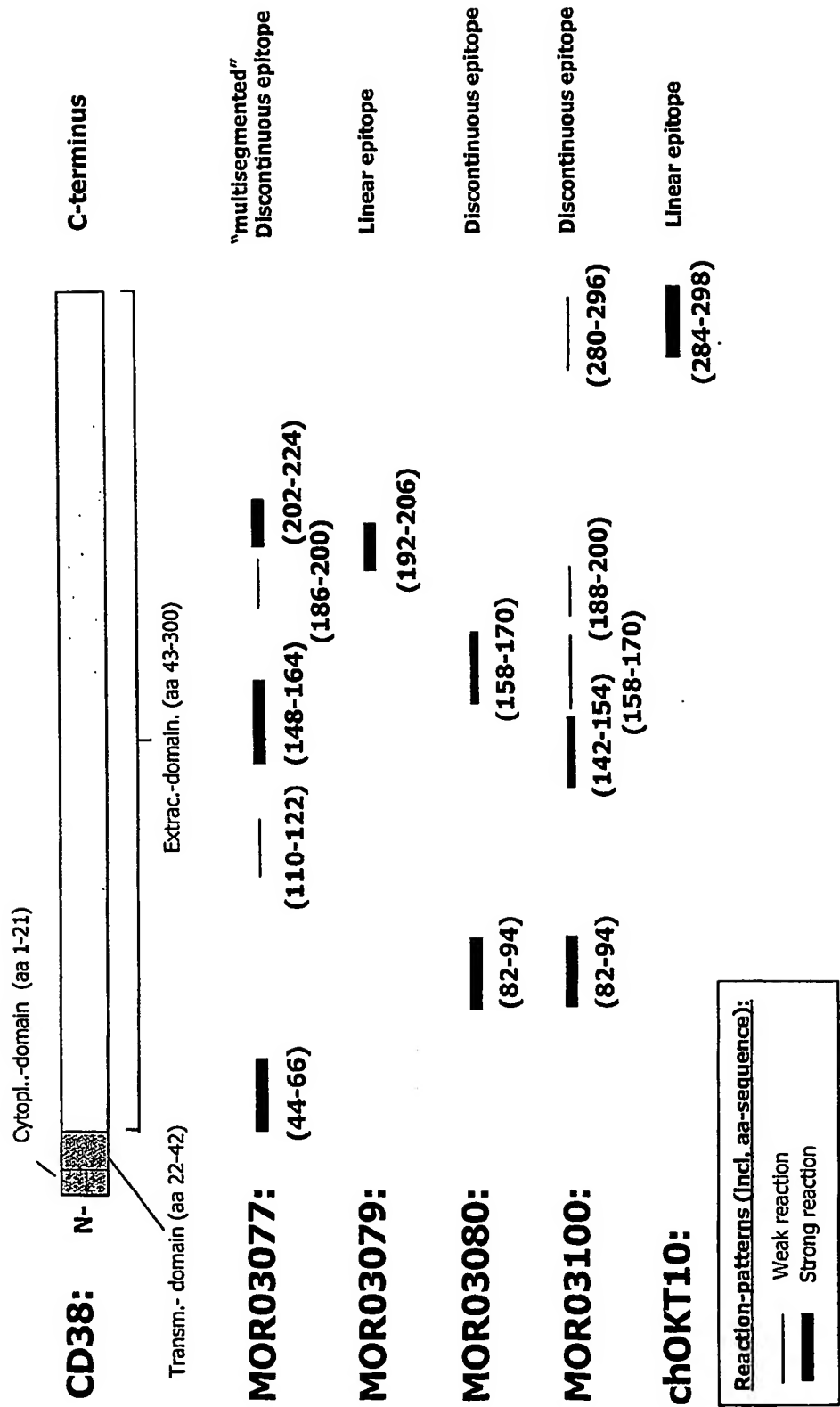


Figure 8: DNA sequence of pMOPRH[®]_h_IgG1_1

```

          StyI
          -----
601   TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
      AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

                                     AatII
                                     -----
651   TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
      ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701   TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
      ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751   ACAAATCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
      TGTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801   GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
      CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

          pMORPH®_Ig_FOR 100.0%
          -----
851   GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
      CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

          M K H L W F F L L L V A A P R

901   GCCACCATGA AACACCTGTG GTTCTTCCTC CTGCTGGTGG CAGCTCCCAG
      CGGTGGTACT TTGTGGACAC CAAGAAGGAG GACGACCACC GTCGAGGGTC

          StyI                      EcoRI                      BlnI
          -----                      -----                      ~
                                     A S T

          W V L S Q V E F C R R L A Q
951   ATGGGTCCTG TCCCAGGTGG AATTCTGCAG GCGGTTAGCT CAGCCTCCAC
      TACCCAGGAC AGGGTCCACC TTAAGACGTC CGCCAATCGA GTCGGAGGTG

          StyI                      BbsI
          -----                      -----
          K G P S V F P L A P S S K S T S G

1001  CAAGGGTCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG AGCACCTCTG
      GTTCCCAGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTTT TCGTGGAGAC

          G T A A L G C L V K D Y F P E P
1051  GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCAGACCG
      CCCCCTGTCTG CCGGGACCCG ACGGACCAGT TCCTGATGAA GGGGCTTGGC

```

V T V S W N S G A L T S G V H T F

1101 GTGACGGTGT CGTGGAAGTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA

P A V L Q S S G L Y S L S S V V T

1151 CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCACCT

V P S S S L G T Q T Y I C N V N

1201 CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT
GGCACGGGAG GTCGTGGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA

StyI

H K P S N T K V D K K V E P K S C

1251 CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG
GTGTTCCGGT CGTTGTGGTT CCACCTGTTT TTTCAACTCG GGTTTAGAAC

D K T H T C P P C P A P E L L G G

1301 TGACAAACT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG
ACTGTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC

BbsI StyI

P S V F L F P P K P K D T L M I

1351 GACCGTCAGT CTTCTCTTC CCCCCAAAC CCAAGGACAC CCTCATGATC
CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG

BbsI

S R T P E V T C V V V D V S H E D

1401 TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA
AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT

BbsI
~

P E V K F N W Y V D G V E V H N A

1451 CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC

K T K P R E E Q Y N S T Y R V V

1501 CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
GGTTCGTGTT CGGCGCCCTC CTCGTCATGT TGTCGTGCAT GGCCACCAG

S V L T V L H Q D W L N G K E Y K

1551 AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
TCGCAGGAGT GGCAGGACGT GGTCCCTGACC GACTTACCGT TCCTCATGTT

C K V S N K A L P A P I E K T I S

1601 GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA

BsrGI

1651 · K A K G Q P R E P Q V Y T L P P
 CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA
 GGTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT

 S R D E L T K N Q V S L T C L V K

 1701 TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
 AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT

 · G F Y P S D I A V E W E S N G Q P

 1751 AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
 TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTG

 · E N N Y K T T P P V L D S D G S
 1801 CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC CGACGGCTCC
 GCCTCTTGTT GATGTTCTGG TCGGAGGGC ACGACCTGAG GCTGCCGAGG

 F F L Y S K L T V D K S R W Q Q G

 1851 TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
 AAGAAGGAGA TGTCGTTCTGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

BbsI

NsiI

· N V F S C S V M H E A L H N H Y T

 1901 GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
 CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

SapI

PmeI

· Q K S L S L S P G K *
 1951 CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGGGCC CGTTTAAACC
 GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTACTCCCGG GCAAATTTGG

 2001 CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
 GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

pMORPH[®] Ig_REV 100.0%

2051 CCCCTCCCCC GTGCCTTCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC
 GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG

+1 A S V V C L L N N F Y P R E A K V
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+1 Q W K V D N A L Q S G N S Q E S
 1101 ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
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+1 V T E Q D S K D S T Y S L S S T L
 1151 TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG
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+1 T L S K A D Y E K H K V Y A C E V
 BspI

 1201 ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT
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+1 T H Q G L S S P V T K S F N R G
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+1 E C *

PmeI

pMORPH^o_Ig_REV 100%

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=
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+2 G A V T V A W K G D S S P V K A G
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+2 V E T T T P S K Q S N N K Y A A S
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+2 S Y L S L T P E Q W K S H R S Y
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+2 S C Q V T H E G S T V E K T V A P
 BbsI

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 CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

+2 T E C S *

PmeI

1301 ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
 TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA

pM_Ig_REV 100%

=====

1351 GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
 CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
 pM_Ig_REV 100.0%

=====

Fig. 11: Proliferation Assay

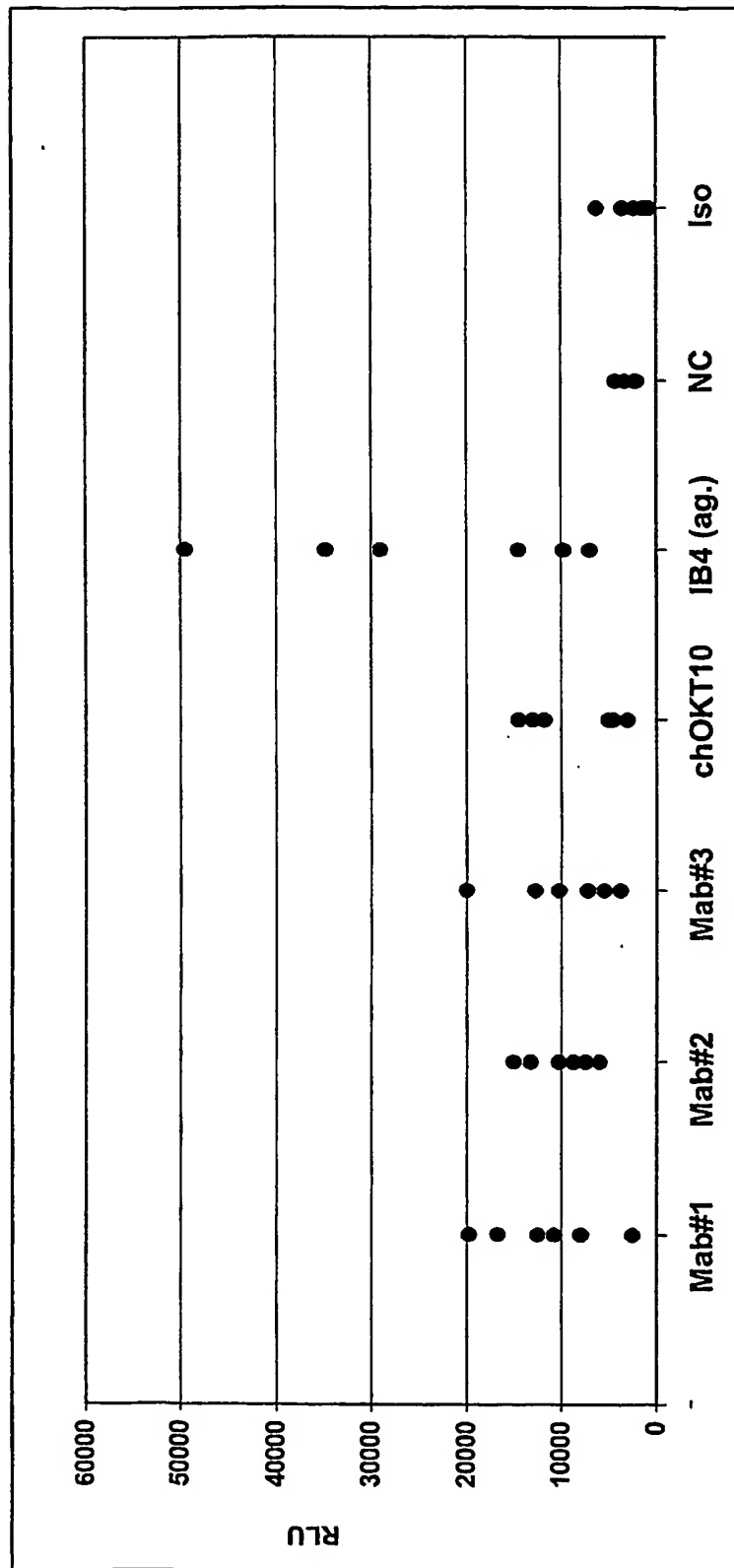


Fig. 12: IL-6 Release Assay

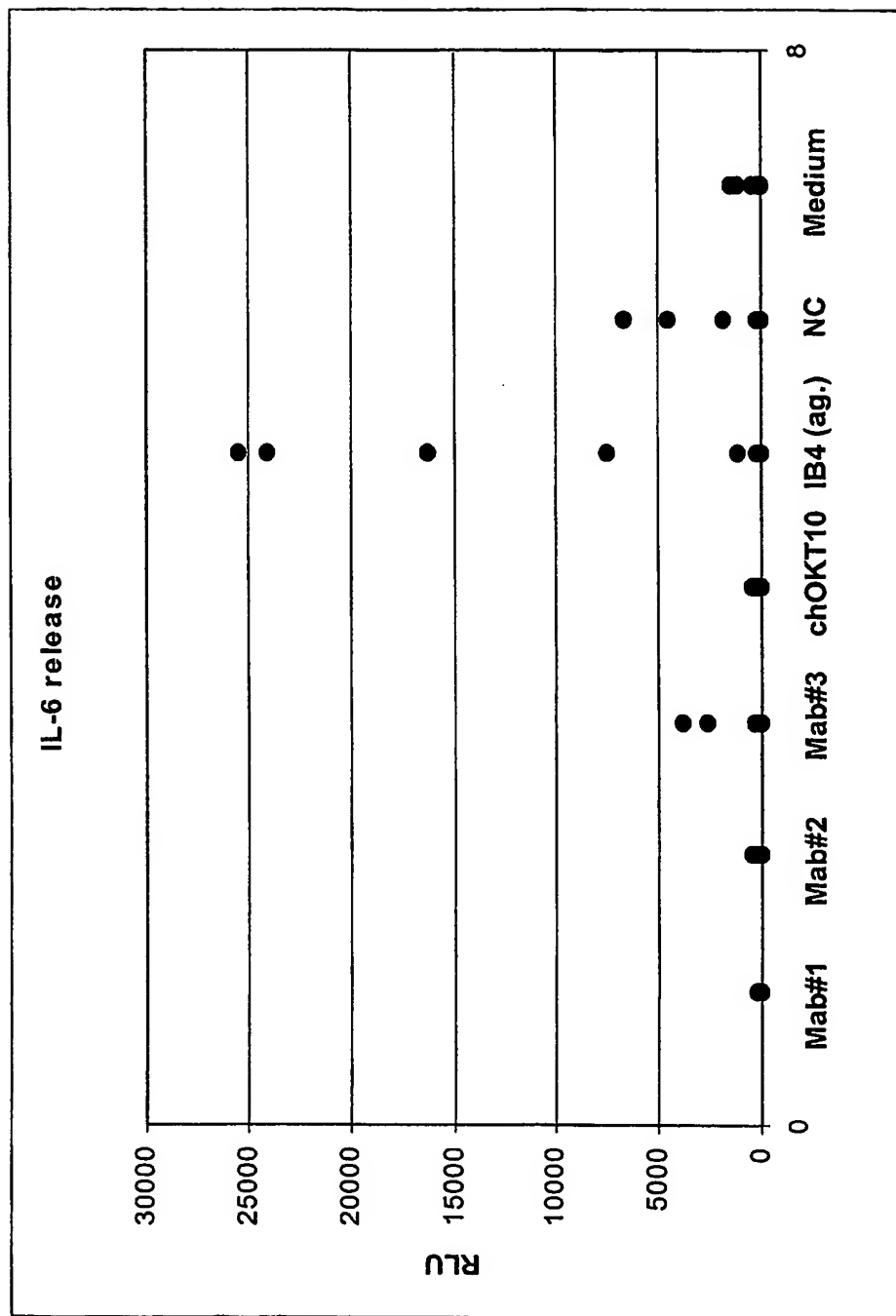


Fig. 13: Cytotoxicity towards CD34+/CD38+ progenitor cells

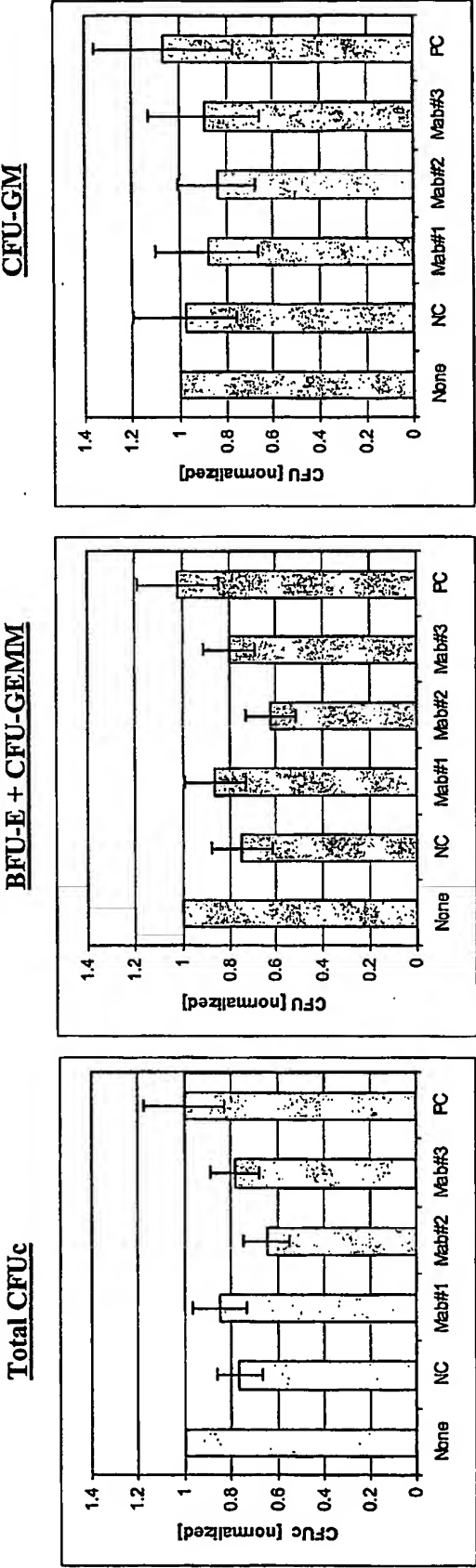


Fig. 14: ADCC with different cell-lines

Cell line	Culture Collection	Origin	Expression [MFI]	Max. specific killing [%] in ADCC ^{a,c}			
				Mab#1	Mab#2	Mab#3	PC
RPMI 8226	ATCC GCL-155	MM	405.71	56	58	54	46
KMS-12-BM	DSMZ ACC551	MM	142.29	26	32	30	34
NCI-H929	ECACC95050415	MM	45.01	68	73	38	54
OPM-2	DSMZ ACC50	MM	37.99	6	13	3	7
U-266	ECACC85051003	MM	26.14	17	14	12	16
KMS-11	Namba et al., 1989 ^b	MM	26.81 ^d	22	30	26	28
JVM-13	DSMZACC19	CLL	463.93	11	20	12	15
JVM-2	DSMZACC12	CLL	140.84	22	28	10	24
CCRF-CEM	ECACC85112105	ALL	301.46	24	29	20	22
Jurkat	DSMZ ACC282	ALL	202.99	7	8	13	12
AML-193	DSMZ ACC549	AML	62.69 ^d	33	26	39	33
OCI-AML5	DSMZ ACC247	AML	207.55 ^d	20	21	16	26
NB-4	DSMZ ACC207	AML	164.7 ^d	36	38	32	37
THP-1	DSMZ ACC16	AML	34.41	64	59	38	43
HL-60 ^d	DSMZ ACC3	AML	18.43 ^d	29	35	29	29
Raji	Burkitt's Lymph.	Burkitt's lymph.	n.d.	53	62	48	n.d.

Fig. 15: ADCC with MM-samples

Antibodies		Mab#1	Mab#2	Mab#3	PC
Parameters:					
MM samples: EC50 [nM] ^a :		0.116-0.202	0.006-0.185	0.027-0.249	0.282-0.356
MM samples: Max spec. killing [%]		13.1 - 61.6	16.2 - 57.9	13.6 - 36.0	15.5 - 49.5

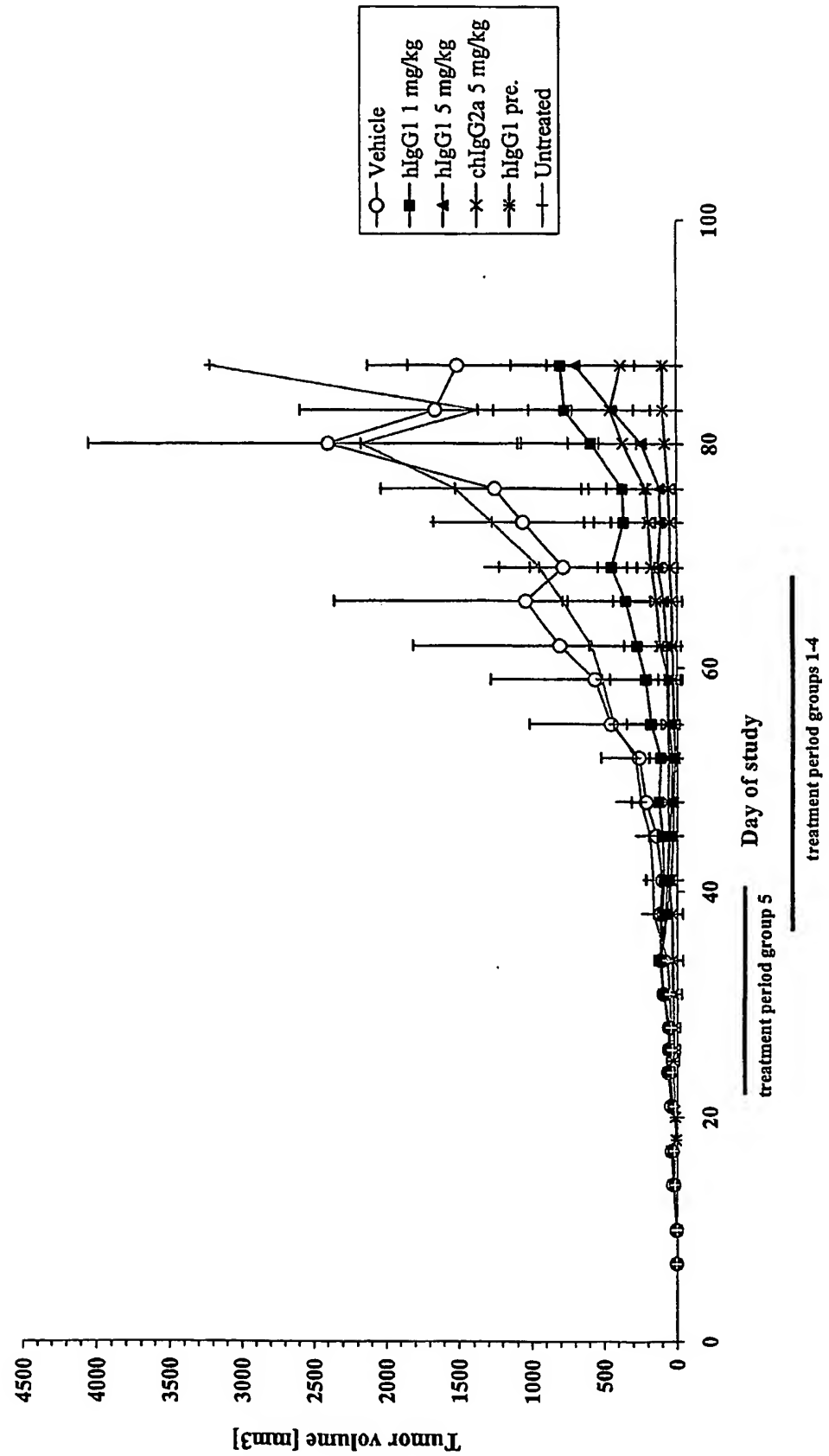


Fig. 16: Treatment of human myeloma xenograft with MOR03080